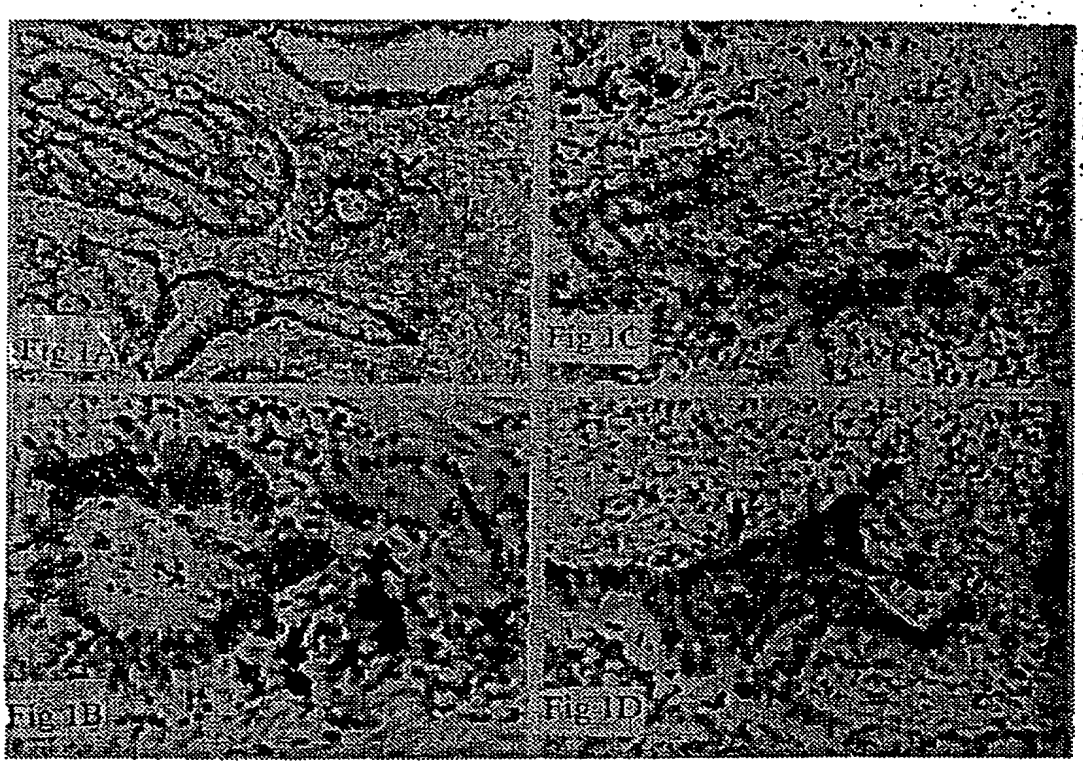


Fig. 1

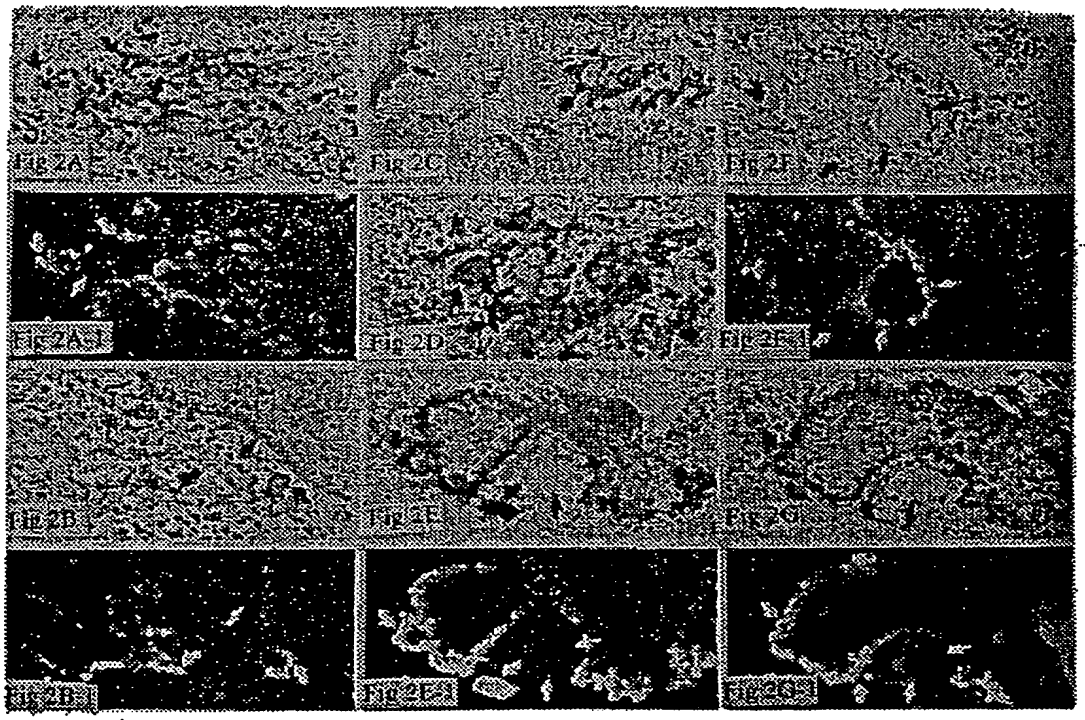
Fig 2A
Fig 2C
Fig 2F
Fig 2A-1
Fig 2D-1
Fig 2F-1
Fig 2B
Fig 2E
Fig 2G
Fig 2B-1
Fig 2E-1
Fig 2G-1

Fig. 2

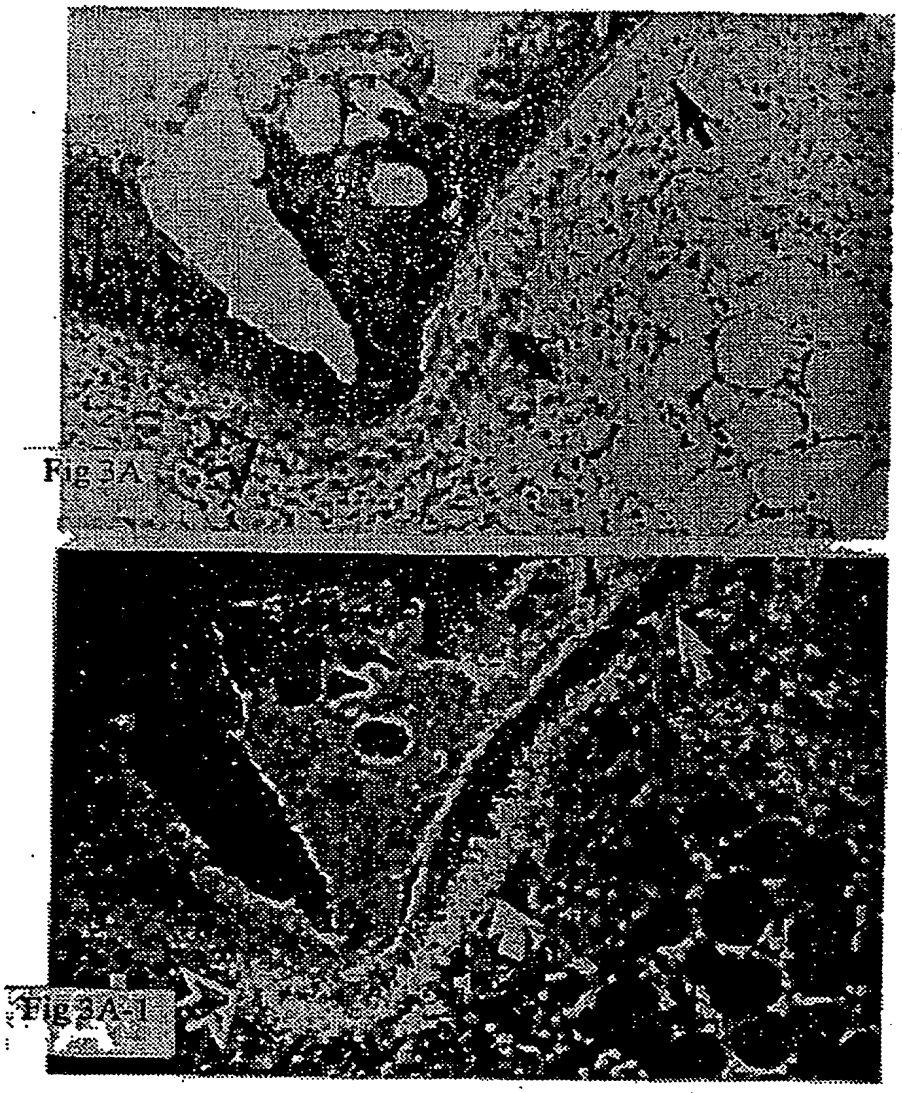


Fig. 3

**FIG 4A** (SEQ ID NO.:12 & 13)

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 1 gaccacctga tcgaaggaaa aggaaggcac agcggagcgc agagtgagaa ccaccaaccg
61 aggcgccggg cagcgacccc tgcagcggag acagagactg agcggcccgg caccgccatg
 1                                                                 M
121 cctgcgctct ggctgggctg ctgcctctgc ttctcgctcc tcctgcccgc agcccgggcc
  2  P  A  L   W  L  G  C   C  L  C   F  S  L   L  L  P  A   A  R  A
181 acctccagga gggaagtctg tgattgcaat gggaagtcca ggcagtgtat ctttgatcgg
 22  T  S  R   R  E  V  C   D  C  N   G  K  S   R  Q  C  I   F  D  R
                          ⇦ Domain V
241 gaacttcaca gacaaactgg taatggattc cgctgcctca actgcaatga caacactgat
 42  E  L  H   R  Q  T  G   N  G  F   R  C  L   N  C  N  D   N  T  D
301 ggcattcact gcgagaagtg caagaatggc ttttaccggc acagagaaag ggaccgctgt
 62  G  I  H   C  E  K  C   K  N  G   F  Y  R   H  R  E  R   D  R  C
361 ttgccctgca attgtaactc caaaggttct cttagtgctc gatgtgacaa ctctggacgg
 82  L  P  C   N  C  N  S   K  G  S   L  S  A   R  C  D  N   S  G  R
421 tgcagctgta aaccaggtgt gacaggagcc agatgcgacc gatgtctgcc aggcttccac
102  C  S  C   K  P  G  V   T  G  A   R  C  D   R  C  L  P   G  F  H
481 atgctcacgg atgcggggtg cacccaagac cagagactgc tagactccaa gtgtgactgt
122  M  L  T   D  A  G  C   T  Q  D   Q  R  L   L  D  S  K   C  D  C
541 gacccagctg gcatcgcagg gccctgtgac gcgggccgct gtgtctgcaa gccagctgtt
142  D  P  A   G  I  A  G   P  C  D   A  G  R   C  V  C  K   P  A  V
601 actggagaac gctgtgatag gtgtcgatca ggttactata atctggatgg ggggaaccct
162  T  G  E   R  C  D  R   C  R  S   G  Y  Y   N  L  D  G   G  N  P
661 gagggctgta cccagtgttt ctgctatggg cattcagcca gctgccgcag ctctgcagaa
182  E  G  C   T  Q  C  F   C  Y  G   H  S  A   S  C  R  S   S  A  E
                                                    ⇦ Domain IV
721 tacagtgtcc ataagatcac ctctaccttt catcaagatg ttgatggctg gaaggctgtc
202  Y  S  V   H  K  I  T   S  T  F   H  Q  D   V  D  G  W   K  A  V
781 caacgaaatg ggtctcctgc aaagctccaa tggtcacagc gccatcaaga tgtgtttagc
222  Q  R  N   G  S  P  A   K  L  Q   W  S  Q   R  H  Q  D   V  F  S
841 tcagcccaac gactagatcc tgtctatttt gtggctcctg ccaaatttct tgggaatcaa
242  S  A  Q   R  L  D  P   V  Y  F   V  A  P   A  K  F  L   G  N  Q
901 caggtgagct atgggcaaag cctgtccttt gactaccgtg tggacagagg aggcagacac
262  Q  V  S   Y  G  Q  S   L  S  F   D  Y  R   V  D  R  G   G  R  H
961 ccatctgccc atgatgtgat cctggaaggt gctggtctac ggatcacagc tcccttgatg
282  P  S  A   H  D  V  I   L  E  G   A  G  L   R  I  T  A   P  L  M
1021 ccacttggca agacactgcc ttgtgggctc accaagactt acacattcag gttaaatgag
302  P  L  G   K  T  L  P   C  G  L   T  K  T   Y  T  F  R   L  N  E
1081 catccaagca ataattggag cccccagctg agttactttg agtatcgaag gttactgcgg
322  H  P  S   N  N  W  S   P  Q  L   S  Y  F   E  Y  R  R   L  L  R
1141 aatctcacag ccctccgcat ccgagctaca tatggagaat acagtactgg gtacattgac
342  N  L  T   A  L  R  I   R  A  T   Y  G  E   Y  S  T  G   Y  I  D
1201 aatgtgaccc tgatttcagc ccgccctgtc tctggagccc cagcaccctg ggttgaacag
362  N  V  T   L  I  S  A   R  P  V   S  G  A   P  A  P  W   V  E  Q
1261 tgtatatgtc ctgttgggta caaggggcaa ttctgccagg attgtgcttc tggctacaag
382  C  I  C   P  V  G  Y   K  G  Q   F  C  Q   D  C  A  S   G  Y  K
     ⇦ Domain III
1321 agagattcag cgagactggg gccttttggc acctgtattc cttgtaactg tcaaggggga
402  R  D  S   A  R  L  G   P  F  G   T  C  I   P  C  N  C   Q  G  G
1381 ggggcctgtg atccagacac aggagattgt tattcagggg atgagaatcc tgacattgag
422  G  A  C   D  P  D  T   G  D  C   Y  S  G   D  E  N  P   D  I  E
1441 tgtgctgact gcccaattgg tttctacaac gatccgcacg acccccgcag ctgcaagcca
442  C  A  D   C  P  I  G   F  Y  N   D  P  H   D  P  R  S   C  K  P
1501 tgtccctgtc ataacgggtt cagctgctca gtgattccgg agacggagga ggtggtgtgc
462  C  P  C   H  N  G  F   S  C  S   V  I  P   E  T  E  E   V  V  C
```

**FIG 4B**

(SEQ ID NO.:12 & 13)

```
1561 aataactgcc ctcccggggt caccggtgcc cgctgtgagc tctgtgctga tggctacttt
 482  N  N  C   P  P  G  V   T  G  A   R  C  E   L  C  A  D   G  Y  F
1621 ggggacccct ttggtgaaca tggcccagtg aggccttgtc agccctgtca atgcaacagc
 502  G  D  P   F  G  E  H   G  P  V   R  P  C   Q  P  C  Q   C  N  S
1681 aatgtggacc ccagtgcctc tgggaattgt gaccggctga caggcaggtg tttgaagtgt
 522  N  V  D   P  S  A  S   G  N  C   D  R  L   T  G  R  C   L  K  C
1741 atccacaaca cagccggcat ctactgcgac cagtgcaaag caggctactt cggggaccca
 542  I  H  N   T  A  G  I   Y  C  D   Q  C  K   A  G  Y  F   G  D  P
1801 ttggctccca acccagcaga caagtgtcga gcttgcaact gtaacccccat gggctcagag
 562  L  A  P   N  P  A  D   K  C  R   A  C  N   C  N  P  M   G  S  E
1861 cctgtaggat gtcgaagtga tggcacctgt gtttgcaagc caggatttgg tggccccaac
 582  P  V  G   C  R  S  D   G  T  C   V  C  K   P  G  F  G   G  P  N
1921 tgtgagcatg gagcattcag ctgtccagct tgctataatc aagtgaagat tcagatggat
 602  C  E  H   G  A  F  S   C  P  A   C  Y  N   Q  V  K  I   Q  M  D
                                 ⁞⇐ Domain I/II
1981 cagtttatgc agcagcttca gagaatggag gccctgattt caaaggctca gggtggtgat
 622  Q  F  M   Q  Q  L  Q   R  M  E   A  L  I   S  K  A  Q   G  G  D
2041 ggagtagtac ctgatacaga gctggaaggc aggatgcagc aggctgagca ggcccttcag
 642  G  V  V   P  D  T  E   L  E  G   R  M  Q   Q  A  E  Q   A  L  Q
2101 gacattctga gagatgccca gatttcagaa ggtgctagca gatcccttgg tctccagttg
 662  D  I  L   R  D  A  Q   I  S  E   G  A  S   R  S  L  G   L  Q  L
2161 gccaaggtga ggagccaaga gaacagctac cagagccgcc tggatgacct caagatgact
 682  A  K  V   R  S  Q  E   N  S  Y   Q  S  R   L  D  D  L   K  M  T
2221 gtggaaagag ttcgggctct gggaagtcag taccagaacc gagttcggga tactcacagg
 702  V  E  R   V  R  A  L   G  S  Q   Y  Q  N   R  V  R  D   T  H  R
2281 ctcatcactc agatgcagct gagcctggca gaaagtgaag cttccttggg aaacactaac
 722  L  I  T   Q  M  Q  L   S  L  A   E  S  E   A  S  L  G   N  T  N
2341 attcctgcct cagaccacta cgtggggcca aatggcttta aaagtctggc tcaggaggcc
 742  I  P  A   S  D  H  Y   V  G  P   N  G  F   K  S  L  A   Q  E  A
2401 acaagattag cagaaagcca cgttgagtca gccagtaaca tggagcaact gacaagggaa
 762  T  R  L   A  E  S  H   V  E  S   A  S  N   M  E  Q  L   T  R  E
2461 actgaggact attccaaaca agccctctca ctggtgcgca aggccctgca tgaaggagtc
 782  T  E  D   Y  S  K  Q   A  L  S   L  V  R   K  A  L  H   E  G  V
2521 ggaagcggaa gcggtagccc ggacggtgct gtggtgcaag ggcttgtgga aaaattggag
 802  G  S  G   S  G  S  P   D  G  A   V  V  Q   G  L  V  E   K  L  E
2581 aaaaccaagt ccctggccca gcagttgaca agggaggcca ctcaagcgga aattgaagca
 822  K  T  K   S  L  A  Q   Q  L  T   R  E  A   T  Q  A  E   I  E  A
2641 gataggtctt atcagcacag tctccgcctc ctggattcag tgtctccgct tcagggagtc
 842  D  R  S   Y  Q  H  S   L  R  L   L  D  S   V  S  P  L   Q  G  V
2701 agtgatcagt cctttcaggt ggaagaagca aagaggatca aacaaaaagc ggattcactc
 862  S  D  Q   S  F  Q  V   E  E  A   K  R  I   K  Q  K  A   D  S  L
2761 tcaagcctgg taaccaggca tatggatgag ttcaagcgta cacaaaagaa tctgggaaac
 882  S  S  L   V  T  R  H   M  D  E   F  K  R   T  Q  K  N   L  G  N
2821 tggaaagaag aagcacagca gctcttacag aatggaaaaa gtgggagaga gaaatcagat
 902  W  K  E   E  A  Q  Q   L  L  Q   N  G  K   S  G  R  E   K  S  D
2881 cagctgcttt cccgtgccaa tcttgctaaa agcagagcac aagaagcact gagtatgggc
 922  Q  L  L   S  R  A  N   L  A  K   S  R  A   Q  E  A  L   S  M  G
2941 aatgccactt tttatgaagt tgagagcatc cttaaaaacc tcagagagtt tgacctgcag
 942  N  A  T   F  Y  E  V   E  S  I   L  K  N   L  R  E  F   D  L  Q
3001 gtggacaaca gaaaagcaga agctgaagaa gccatgaaga gactctccta catcagccag
 962  V  D  N   R  K  A  E   A  E  E   A  M  K   R  L  S  Y   I  S  Q
3061 aaggtttcag atgccagtga caagacccag caagcagaaa gagccctggg gagcgctgct
 982  K  V  S   D  A  S  D   K  T  Q   Q  A  E   R  A  L  G   S  A  A
3121 gctgatgcac agagggcaaa gaatggggcc ggggaggccc tggaaatctc cagtgagatt
1002  A  D  A   Q  R  A  K   N  G  A   G  E  A   L  E  I  S   S  E  I
```

**FIG 4C**

(SEQ ID NO.:12 & 13)

```
3181 gaacaggaga ttgggagtct gaacttggaa gccaatgtga cagcagatgg agccttggcc
1022  E  Q  E   I  G  S  L   N  L  E   A  N  V   T  A  D  G   A  L  A
3241 atggaaaagg gactggcctc tctgaagagt gagatgaggg aagtggaagg agagctggaa
1042  M  E  K   G  L  A  S   L  K  S   E  M  R   E  V  E  G   E  L  E
3301 aggaaggagc tggagtttga cacgaatatg gatgcagtac agatggtgat tacagaagcc
1062  R  K  E   L  E  F  D   T  N  M   D  A  V   Q  M  V  I   T  E  A
3361 cagaaggttg ataccagagc caagaacgct ggggttacaa tccaagacac actcaacaca
1082  Q  K  V   D  T  R  A   K  N  A   G  V  T   I  Q  D  T   L  N  T
3421 ttagacggcc tcctgcatct gatggaccag cctctcagtg tagatgaaga ggggctggtc
1102  L  D  G   L  L  H  L   M  D  Q   P  L  S   V  D  E  E   G  L  V
3481 ttactggagc agaagctttc ccgagccaag acccagatca acagccaact gcggcccatg
1122  L  L  E   Q  K  L  S   R  A  K   T  Q  I   N  S  Q  L   R  P  M
3541 atgtcagagc tggaagagag ggcacgtcag cagaggggcc acctccattt gctggagaca
1142  M  S  E   L  E  E  R   A  R  Q   Q  R  G   H  L  H  L   L  E  T
3601 agcatagatg ggattctggc tgatgtgaag aacttggaga acattaggga caacctgccc
1162  S  I  D   G  I  L  A   D  V  K   N  L  E   N  I  R  D   N  L  P
3661 ccaggctgct acaataccca ggctcttgag caacagtgaa gctgccataa atatttctca
1182  P  G  C   Y  N  T  Q   A  L  E   Q  Q  *

3721 actgaggttc ttgggataca gatctcaggg ctcgggagcc atgtcatgtg agtgggtggg
3781 atggggacat ttgaacatgt ttaatgggta tgctcaggtc aactgacctg accccattcc
3841 tgatcccatg gccaggtggt tgtcttattg caccatactc cttgcttcct gatgctgggc
3901 atgaggcaga taggcactgg tgtgagaatg atcaaggatc tggaccccaa agatagactg
3961 gatggaaaga caaactgcac aggcagatgt ttgcctcata atagtcgtaa gtggagtcct
4021 ggaatttgga caagtgctgt tgggatatag tcaacttatt ctttgagtaa tgtgactaaa
4081 ggaaaaaact ttgactttgc ccaggcatga aattcttcct aatgtcagaa cagagtgcaa
4141 cccagtcaca ctgtggccag taaaatacta ttgcctcata ttgtcctctg caagcttctt
4201 gctgatcaga gttcctccta cttacaaccc agggtgtgaa catgttctcc attttcaagc
4261 tggaagaagt gagcagtgtt ggagtgagga cctgtaaggc aggcccattc agagctatgg
4321 tgcttgctgg tgcctgccac cttcaagttc tggacctggg catgacatcc tttcttttaa
4381 tgatgccatg gcaacttaga gattgcattt ttattaaagc atttcctacc agcaaagcaa
4441 atgttgggaa agtatttact ttttcggttt caaagtgata gaaaagtgtg gcttgggcat
4501 tgaaagaggt aaaattctct agatttatta gtcctaattc aatcctactt ttcgaacacc
4561 aaaaatgatg cgcatcaatg tattttatct tattttctca atctcctctc tctttcctcc
4621 acccataata agagaatgtt cctactcaca cttcagctgg gtcacatcca tccctccatt
4681 catccttcca tccatctttc catccattac ctccatccat ccttccaaca tatatttatt
4741 gagtacctac tgtgtgccag gggctggtgg gacagtggtg acatagtctc tgccctcata
4801 gagttgattg tctagtgagg aagacaagca tttttaaaaa ataaatttaa acttacaaac
4861 tttgtttgtc acaagtggtg tttattgcaa taaccgcttg gtttgcaacc tctttgctca
4921 acagaacata tgttgcaaga ccctcccatg ggcactgagt ttggcaagga tgacagagct
4981 ctgggttgtg cacatttctt tgcattccag cgtcactctg tgccttctac aactgattgc
5041 aacagactgt tgagttatga taacaccagt gggaattgct ggaggaacca gaggcacttc
5101 caccttggct gggaagacta tggtgctgcc ttgcttctgt atttccttgg attttcctga
5161 aagtgttttt aaataaagaa caattgttag atgccaaaaa  //
```

**FIG 4D**

(SEQ ID NO.:14 & 15)

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3421 ttagacggcc tcctgcatct gatgggtatg tgaacccaca acccacaacc ttccagctcc
1102  L  D  G   L  L  H  L   M  G  M   *

3481 atgctccagg gctttgctcc agaacactca ctatacctag ccccagcaaa ggggagtctc
3541 agctttcctt aaggatatca gtaaatgtgc tttgtttcca ggcccagata actttcggca
3601 ggttccctta catttactgg accctgtttt accgttgcta agatgggtca ctgaacacct
3661 attgcacttg ggggtaaagg tctgtgggcc aaagaacagg tgtatataag caacttcaca
3721 gaacacgaga cagcttggga atcctgctaa agagtctggc ctggaccctg agaagccagt
3781 ggacagtttt aagcagagga ataacatcac cactgtatat ttcagaaaga tcactagggc
3841 agccgagtgg aggaaagctt gaagaggggg ttagagagaa ggcaggttga gactacttaa
3901 gatattgttg aaataattga agagagaaat gacaggagcc tgctctaagg cagtagaatg
3961 gtggctggga agatgtgaag gaagattttc ccagtctgtg aagtcaagaa tcacttgccg
4021 gccgggtgtg gtggctcacg cctgtaattc tagcactttg ggagactgaa gcgggtggat
4081 cacccgaggt caggagttga agaccagcct ggccaacatg gtgaaaccct gtctctacta
4141 aaagtacaaa aattagctgg atgatggtgg tgggcgcctg taattccagc tactcaggag
4201 tctgaggcag gagaatcgct tgaacccagg aggcgaggtt acagtgagcc aagattgcac
4261 cactgctctt ccagcctggg aacagagaga ctgcctaaaa aaaaaaaaaa aaaaaa  //
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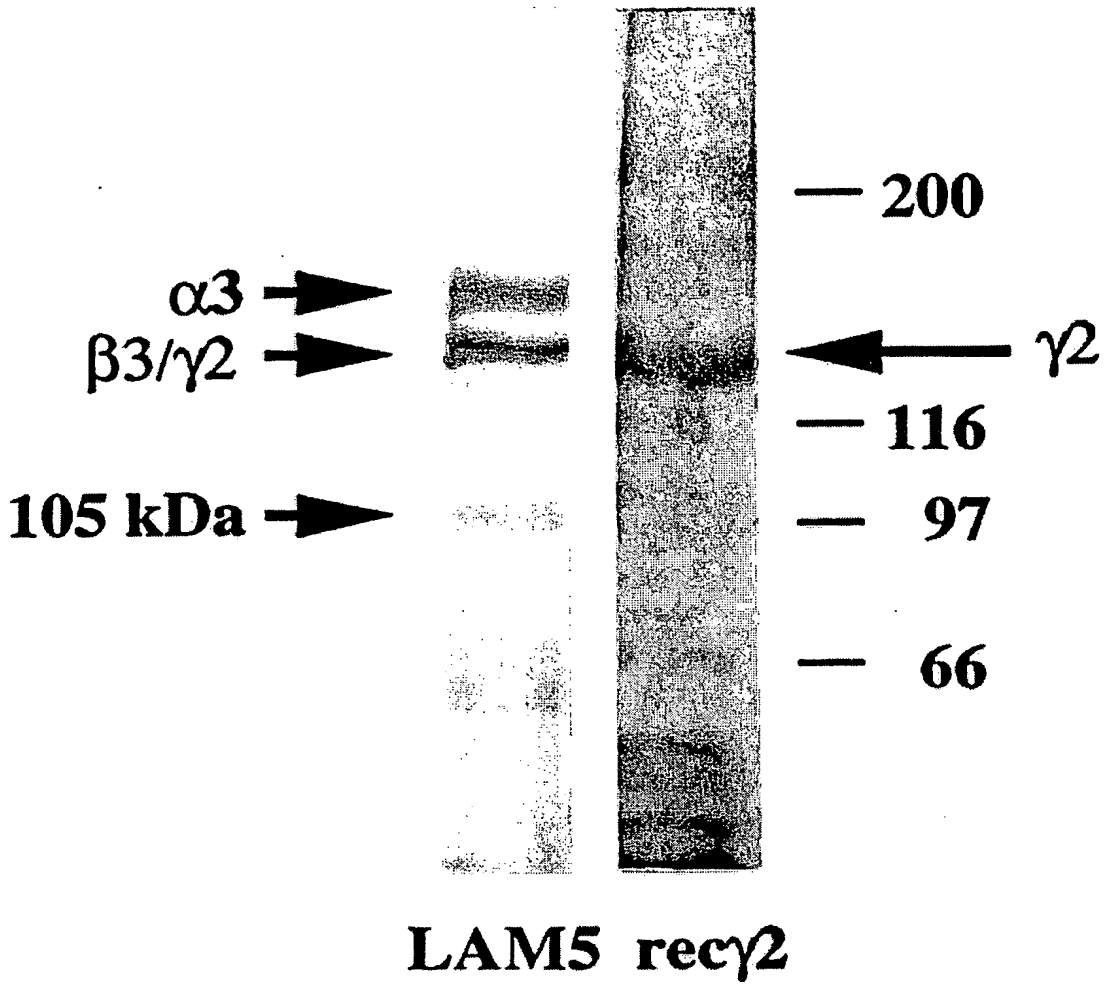


Fig. 5

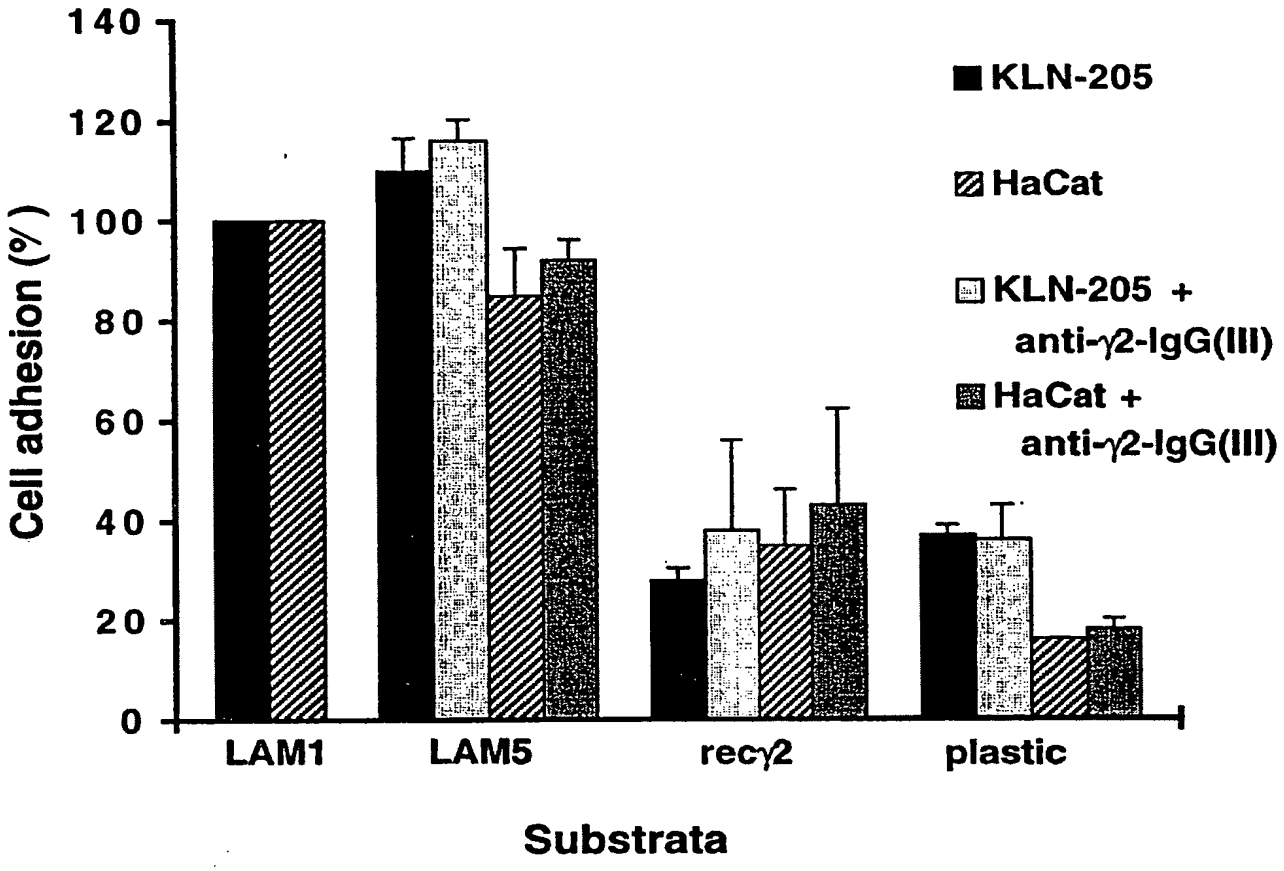
140
120
100
80
60
40
20
0
Cell adhesion (%)
KLN-205
HaCat
KLN-205 + anti-γ2-IgG(III)
HaCat + anti-γ2-IgG(III)
LAM1
LAM5
recγ2
plastic
Substrata

Fig. 6

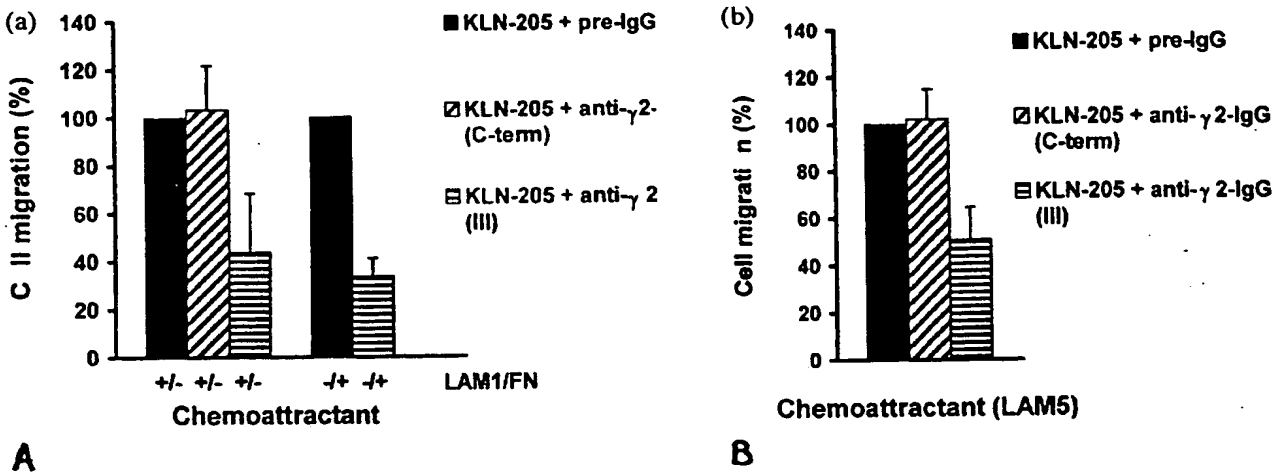
(a)
140
120
100
80
60
40
20
0
C ll mlgration (%)
KLN-205 + pre-IgG
KLN-205 + anti-γ2-
(C-term)
KLN-205 + anti-γ 2
(III)
+/- +/- +/- -/+ -/+
LAM1/FN
Chemoattractant
A
(b)
140
120
100
80
60
40
20
0
Cell migrati n (%)
KLN-205 + pre-IgG
KLN-205 + anti-γ2-IgG
(C-term)
KLN-205 + anti-γ 2-IgG
(III)
Chemoattractant (LAM5)
B

Fig 7

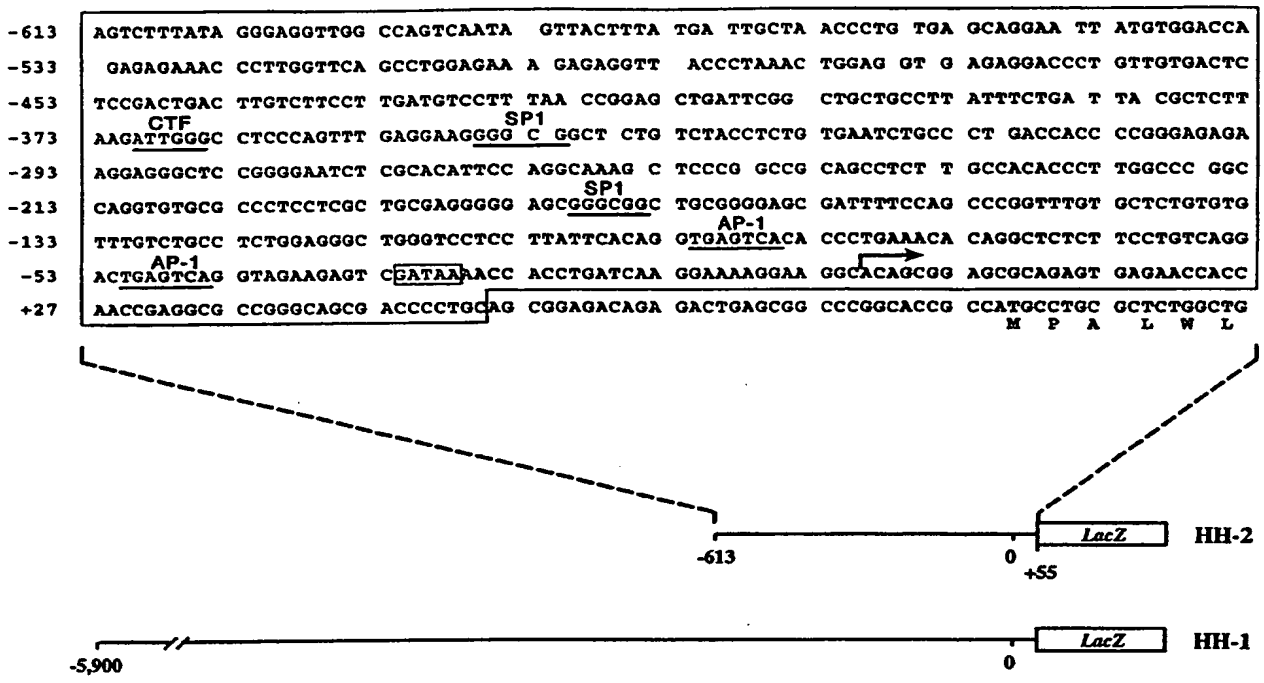
-613 AGTCTTTATA GGGAGGTTGG CCAGTCAATA GTTACTTTA TGA TTGCTA ACCCTG TGA GCAGGAA TT ATGTGGACCA
-533 GAGAGAAAC CCTTGGTTCA GCCTGGAGAA A GAGAGGTT ACCCTAAAC TGGAG GT G AGAGGACCCT GTTGTGACTC
-453 TCCGACTGAC TTGTCTTCCT TGATGTCCTT TAA CCGGAG CTGATTCGG CTGCTGCCTT ATTTCTGA T TA CGCTCTT
-373 AAGATTGGGC CTCCCAGTTT GAGGAAGGGG C GGCT CTG TCTACCTCTG TGAATCTGCC CT GACCACC CCGGGAGAGA
-293 AGGAGGGCTC CGGGGAATCT CGCACATTCC AGGCAAAG C TCCCG GCCG CAGCCTCT T GCCACACCCT TGGCCC GGC
-213 CAGGTGTGCG CCCTCCTCGC TGCGAGGGGG AGCGGGCGGC TGCGGGGAGC GATTTTCCAG CCCGGTTTGT GCTCTGTGTG
-133 TTTGTCTGCC TCTGGAGGGC TGGGTCCTCC TTATTCACAG GTGAGTCACA CCCTGAAACA CAGGCTCTCT TCCTGTCAGG
-53 ACTGAGTCAG GTAGAAGAGT CGATAAAACC ACCTGATCAA GGAAAAGGAA GGCACAGCGG AGCGCAGAGT GAGAACCACC
+27 AACCGAGGCG CCGGGCAGCG ACCCCTGCAG CGGAGACAGA GACTGAGCGG CCCGGCACCG CCATGCCTGC GCTCTGGCTG
M P A L W L
CTF
SP1
SP1
AP-1
AP-1
-613
0
+55
LacZ
HH-2
-5,900
0
LacZ
HH-1

Fig. 8

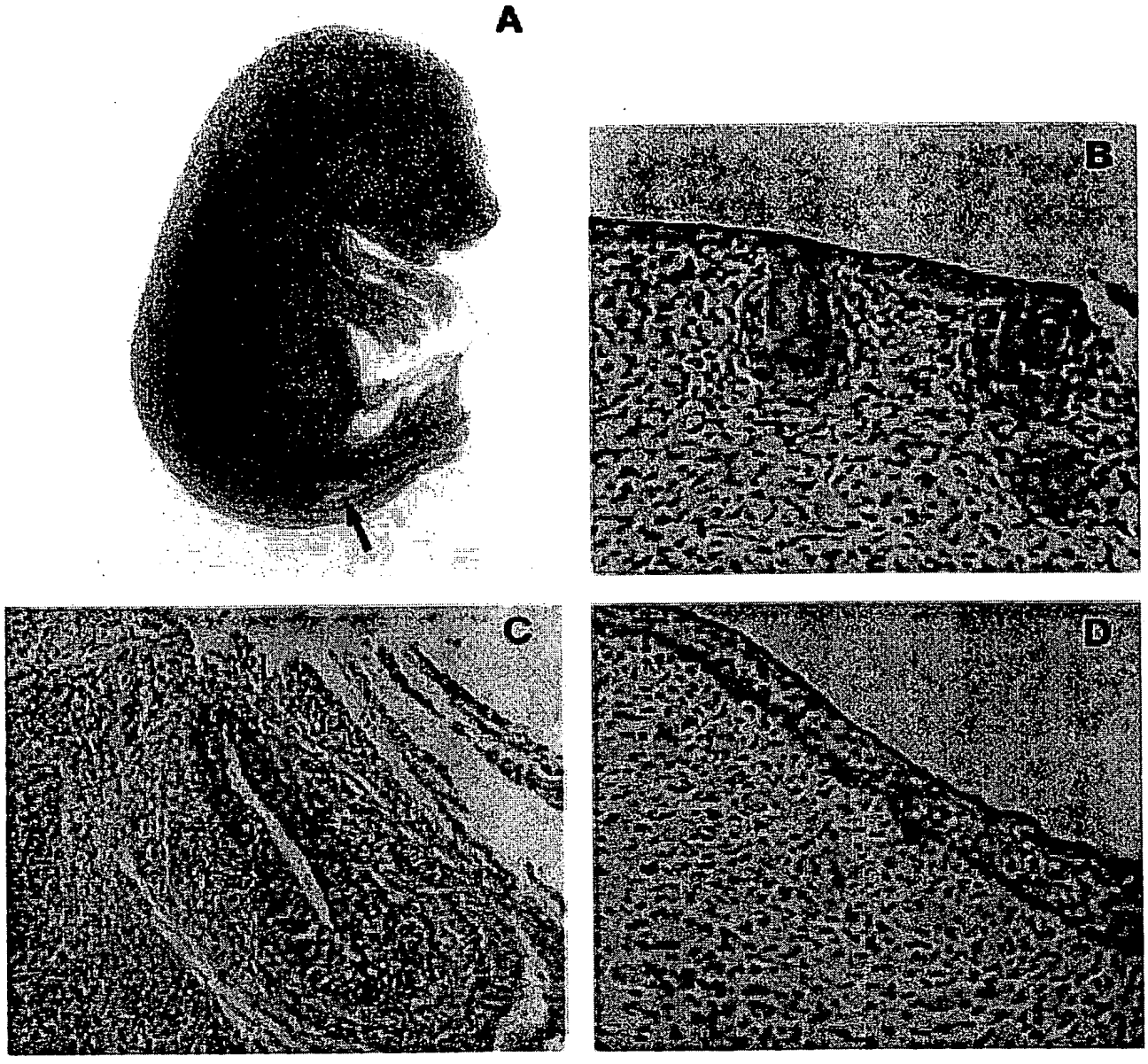


Fig. 9

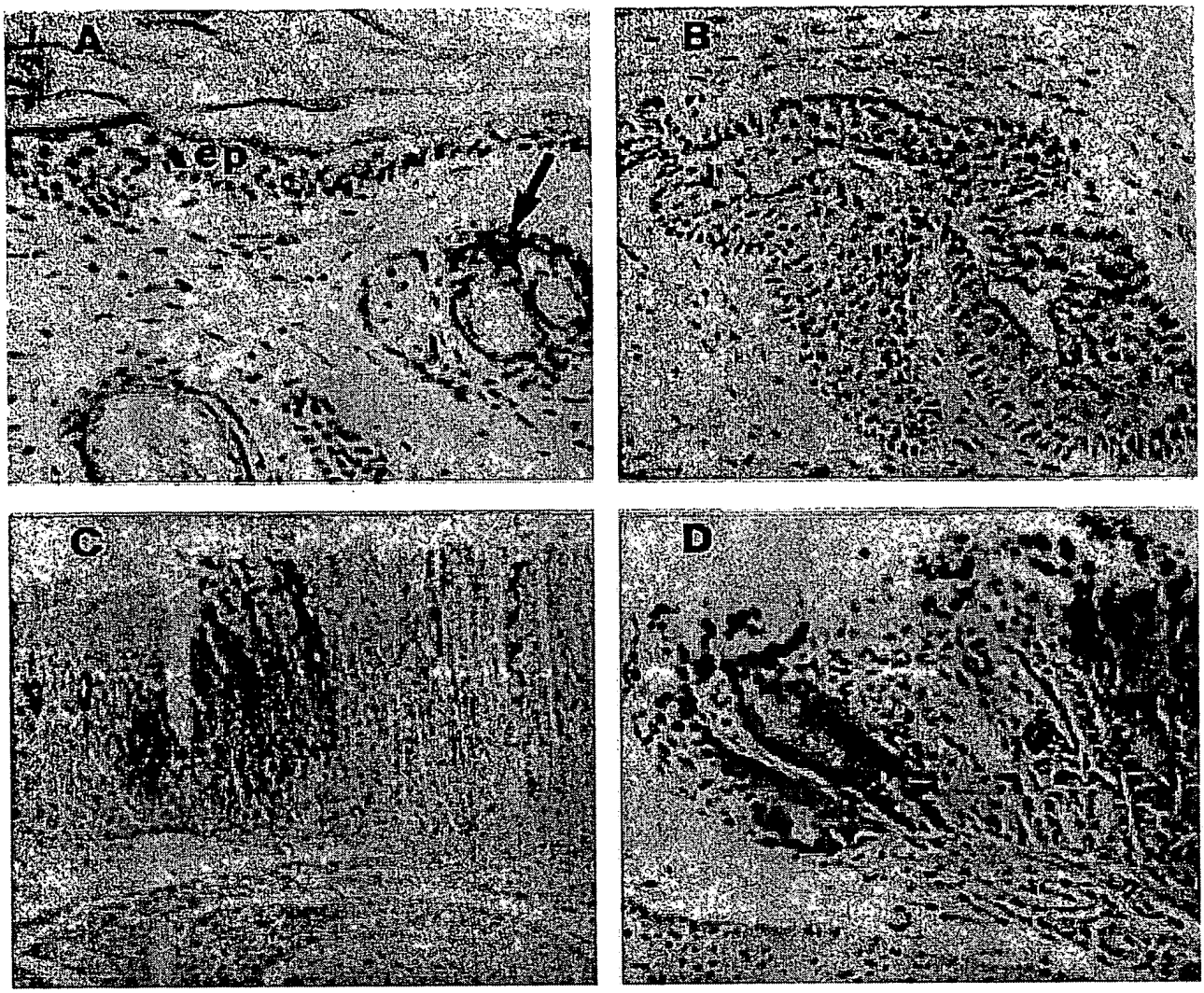


Fig. 10

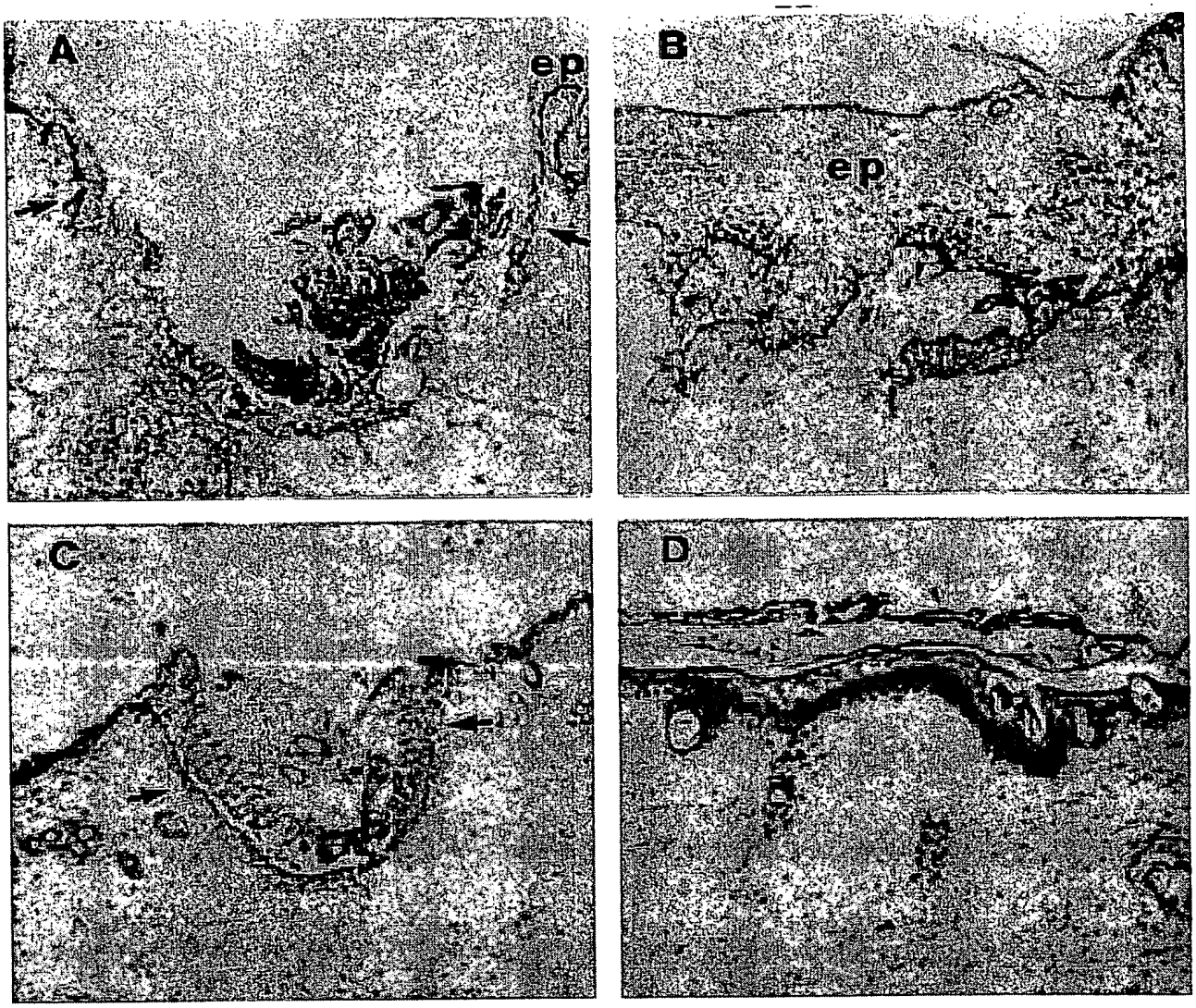


Fig. 11